

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/8.20,339
Source: OIR
Date Processed by STIC: 2/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/820,339

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIKE

RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/820,339

TIME: 14:22:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

Does Not Comply
Corrected Diskette Needed

4-5

3 <110> APPLICANT: FUCHS, Sara
 4 BARCHAN, Dora
 5 SOUROUJON, Miriam
 7 <120> TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR
 AND THEIR USE
 8 FOR TREATMENT OF MYASTHENIA GRAVIS
 10 <130> FILE REFERENCE: FUCHS=2A
 12 <140> CURRENT APPLICATION NUMBER: US/09/820,339
 12 <141> CURRENT FILING DATE: 1999-11-08
 12 <150> PRIOR APPLICATION NUMBER: 09/423,398
 13 <151> PRIOR FILING DATE: 1999-11-08
 15 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00211
 16 <151> PRIOR FILING DATE: 1998-05-06
 18 <160> NUMBER OF SEQ ID NOS: 32
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 630
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
 28 tccgaacatg agaccgctct ggtggcaaag ctatttaaag actacagcag cgtgggtgcgg 60
 30 ccagtggaag accaccgcca ggtcgtggag gtcaccgtgg gcctgcagct gatacagctc 120
 32 atcaatgtgg atgaagtaaa tcagatcgtg acaaccaatg tgcgtctgaa acagcaatgg 180
 34 gtggattaca acctaaaatg gaatccagat gactatggcg gtgtgaaaaa aattcacatt 240
 36 ccttcagaaa agatctggcg cccagacctt gttctctata acgatgcaga tggtagcttt 300
 38 gctattgtca agttcaccaa agtgctcctg cagtacactg gccacatcac gtggacacct 360
 40 ccagccatct ttaaaagcta ctgtgagatc atcgtcaccc actttccctt tgatgaacag 420
 42 aactgcagca tgaagctggg cacctggacc tacgacggct ctgtcgtggc catcaaccg 480
 44 gaaagcgacc agccagacct gagcaacttc atggagagcg gggagtgggt gatcaaggag 540
 46 tcccggggct ggaagcactc cgtgacctat tcctgctgcc ccgacacccc ctacctggac 600
 48 atcacctacc acttcgtcat gcagcgctg 630
 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 210
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Homo sapiens
 56 <400> SEQUENCE: 2
 58 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser
 59 1 5 10 15
 61 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr
 62 20 25 30
 64 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
 65 35 40 45
 67 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp Val Asp Tyr Asn
 68 50 55 60
 70 Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys Lys Ile His Ile
 71 65 70 75 80
 73 Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu Tyr Asn Asn Ala
 74 85 90 95

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/820,339

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Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

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76 Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val Leu Leu Gln Tyr
77      100      105      110
79 Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys
80      115      120      125
82 Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln Asn Cys Ser Met
83      130      135      140
85 Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val Ala Ile Asn Pro
86 145      150      155      160
88 Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu Ser Gly Glu Trp
89      165      170      175
91 Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val Thr Tyr Ser Cys
92      180      185      190
94 Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His Phe Val Met Gln
95      195      200      205
97 Arg Leu
98      210
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 75
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 3
106 ggtgacatgg tagatctgcc acgccccagc tgcgtgactt tgggagttcc tttgttttct      60
108 catctgcagg atgag                                     75
111 <210> SEQ ID NO: 4
112 <211> LENGTH: 25
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 4
118 Gly Asp Met Val Asp Leu Pro Arg Pro Ser Cys Val Thr Leu Gly Val
119 1      5      10      15
121 Pro Leu Phe Ser His Leu Gln Asp Glu
122      20      25
124 <210> SEQ ID NO: 5
125 <211> LENGTH: 705
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 5
130 tccgaacatg agaccctgtt ggtggcaaag ctattttaag actacagcag cgtgggtgcgg      60
132 ccagtggaaag accaccgcca ggtcgtggag gtcaccgtgg gcctgcagct gatacagctc      120
134 atcaatgttg atgaagtaaa tcagatcgtg acaaccaatg tgcgtctgaa acaggggtgac      180
136 atggtagatc tgccacgccc cagctgcgtg actttgggag ttctttgtt ttctcatctg      240
138 caggatgagc aatgggtgga ttacaacctt aaatggaatc cagatgacta tggcggtgtg      300
140 aaaaaaattc acattccttc agaaaagatc tggcgcccag acctgtttct ctataacgat      360
142 gcagatggtg actttgctat tgtcaagttc accaaagtgc tctgcagta cactggccac      420
144 atcacgtgga cacctccagc catctttaaa agctactgtg agatcatcgt caccactttt      480
146 ccctttgatg aacagaactg cagcatgaag ctgggcacct ggacctacga cggctctgtc      540
148 gtggccatca acccggaag cgaccagcca gacctgagca acttcatgga gageggggag      600
150 tgggtgatca aggagtcccg gggctggaag cactccgtga cctattcctg ctgccccgac      660
152 accccctacc tggacatcac ctaccacttc gtcatgcagc gctctg                                     705

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RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/820,339

TIME: 14:22:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

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155 <210> SEQ ID NO: 6
156 <211> LENGTH: 235
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 6
162 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser
163 1 5 10 15
165 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr
166 20 25 30
168 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
169 35 40 45
171 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu
172 50 55 60
174 Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu
175 65 70 75 80
177 Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp
178 85 90 95
180 Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg
181 100 105 110
183 Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val
184 115 120 125
186 Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr
187 130 135 140
189 Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe
190 145 150 155 160
192 Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr
193 165 170 175
195 Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu
196 180 185 190
198 Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly
199 195 200 205
201 Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu
202 210 215 220
204 Asp Ile Thr Tyr His Phe Val Met Gln Arg Leu
205 225 230 235
207 <210> SEQ ID NO: 7
208 <211> LENGTH: 690
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 7
213 tccgaacatg agaccgcgtct ggtggcaaag ctattttaag actacagcag cgtgggtgcgg 60
215 ccagtggaag accaccgcca ggtcgtggag gtcaccgtgg gcctgcagct gatacagctc 120
217 atcaatgttg atgaagtaaa tcagatcggtg acaaccaatg tgcgtctgaa acagggtgac 180
219 atggttagatc tgccacgccc cagctgcgtg actttgggag ttctttgtt ttctcatctg 240
221 caggatgagc aatgggtgga ttacaacctt aaatggaatc cagatgacta tggcgggtgtg 300
223 aaaaaaattc acattccttc agaaaagatc tggcgccag accttgttct ctataacgat 360
225 gcagatggtg actttgctat tgtcaagttc accaaagtgc tcctgcagta cactggccac 420
227 atcacgtgga cacctccagc catctttaa agctactgtg agatcatcgt caccactttt 480
229 ccctttgatg aacagaactg cagcatgaag ctgggcacct ggacctacga cggctctgtc 540

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RAW SEQUENCE LISTING

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Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

231 gtggccatca acccggaag cgaccagcca gacctgagca acttcatgga gagcggggag 600
 233 tgggtgatca aggagtcccg gggctggaag cactocgtga cctattcctg ctgccccgac 660
 235 accccctacc tggacatcac ctaccacttc 690

238 <210> SEQ ID NO: 8

239 <211> LENGTH: 230

240 <212> TYPE: PRT

241 <213> ORGANISM: Homo sapiens

243 <400> SEQUENCE: 8

245 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser

246 1 5 10 15

248 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr

249 20 25 30

251 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln

252 35 40 45

254 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu

255 50 55 60

257 Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu

258 65 70 75 80

260 Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp

261 85 90 95

263 Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg

264 100 105 110

266 Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val

267 115 120 125

269 Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr

270 130 135 140

272 Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe

273 145 150 155 160

275 Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr

276 165 170 175

278 Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu

279 180 185 190

281 Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly

282 195 200 205

284 Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu

285 210 215 220

287 Asp Ile Thr Tyr His Phe

288 225 230


290 <210> SEQ ID NO: 9

291 <211> LENGTH: 20

292 <212> TYPE: DNA

C--> 293 <213> ORGANISM: Artificial synthetic

W--> 295 <220> FEATURE:

W--> 295 <223> OTHER INFORMATION: 

295 <400> SEQUENCE: 9

296 ccggatccga acatgagacc

299 <210> SEQ ID NO: 10

300 <211> LENGTH: 23

301 <212> TYPE: DNA

(global error)

invalid - see item 10 on Error Summary sheet

Synthetic goes on <223> line.

20

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
TIME: 14:22:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\07272001\I820339.raw

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C--> 302 <213> ORGANISM: Artificial synthetic
W--> 304 <220> FEATURE:
W--> 304 <223> OTHER INFORMATION:
      304 <400> SEQUENCE: 10
      305 cgggaattcca ggcgctgcat gac
      308 <210> SEQ ID NO: 11
      309 <211> LENGTH: 26
      310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial synthetic
W--> 313 <220> FEATURE:
W--> 313 <223> OTHER INFORMATION:
      313 <400> SEQUENCE: 11
      314 cgggaattctg gaggtgtcca cgtgat
      317 <210> SEQ ID NO: 12
      318 <211> LENGTH: 23
      319 <212> TYPE: DNA
C--> 320 <213> ORGANISM: Artificial synthetic
W--> 322 <220> FEATURE:
W--> 322 <223> OTHER INFORMATION:
      322 <400> SEQUENCE: 12
      323 ccggatccgc catctttaaa agc
      326 <210> SEQ ID NO: 13
      327 <211> LENGTH: 25
      328 <212> TYPE: DNA
C--> 329 <213> ORGANISM: Artificial synthetic
W--> 331 <220> FEATURE:
W--> 331 <223> OTHER INFORMATION:
      331 <400> SEQUENCE: 13
      332 ggccatgggc tccgaacatg agacc
      335 <210> SEQ ID NO: 14
      336 <211> LENGTH: 29
      337 <212> TYPE: DNA
C--> 338 <213> ORGANISM: Artificial synthetic
W--> 340 <220> FEATURE:
W--> 340 <223> OTHER INFORMATION:
      340 <400> SEQUENCE: 14
      341 ccggatcctc aaaagtgrta ggtgatrta
      344 <210> SEQ ID NO: 15
      345 <211> LENGTH: 24
      346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial synthetic
W--> 349 <220> FEATURE:
W--> 349 <223> OTHER INFORMATION:
      349 <400> SEQUENCE: 15
      350 cgctatgggg ctgcttggtg acag
      353 <210> SEQ ID NO: 16
      354 <211> LENGTH: 24
      355 <212> TYPE: DNA
C--> 356 <213> ORGANISM: Artificial synthetic

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FBI →

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

DATE: 07/27/2001

PATENT APPLICATION: US/09/820,339

TIME: 14:22:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:293 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:295 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:295 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:304 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:304 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:311 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:313 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:313 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:320 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:322 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:322 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:329 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:331 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:331 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:338 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:340 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:340 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:347 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:349 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:349 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:356 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:358 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:358 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:365 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:367 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:374 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:376 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:376 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:383 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:385 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:385 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:392 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:394 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:394 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:401 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:403 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:403 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:410 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:412 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:412 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:419 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:421 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:421 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24

VERIFICATION SUMMARY

DATE: 07/27/2001

PATENT APPLICATION: US/09/820,339

TIME: 14:22:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

L:430 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:430 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:437 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:439 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:439 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:446 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:448 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:448 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:455 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:457 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:457 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:464 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:475 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:475 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:482 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:484 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:484 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:491 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:493 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:493 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:500 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:502 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:502 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: